

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Thomas, Lawrence J.
- (ii) TITLE OF INVENTION: PLASMID-BASED VACCINE FOR
TREATING ATHEROSCLEROSIS
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Banner & Witcoff, Ltd.
 - (E) STREET: 75 State Street, Suite 2300
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109-1807
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC DOS/MS-DOS
 - (D) SOFTWARE: WordPerfect 6.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: (not yet assigned)
 - (B) FILING DATE: 01 May 1997 (01.05.97)
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION: 08/640,713
 - (B) FILING DATE: 01 May 1996 (01.05.96)
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION: 08/802,967
 - (B) FILING DATE: 21 February 1997 21.02.97
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Leon R. Yankwich
 - (B) REGISTRATION NUMBER: 30,237
 - (C) REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)

(2) INFORMATION FOR SEQ ID NO: 1.

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE: Structural coding sequence for
mature rabbit GETF
 - (A) NAME:
 - (B) LOCATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Nagashima, Mariko, et al.

(B) TITLE: Cloning and mRNA tissue
distribution of rabbit
cholesteryl ester transfer
protein

(C) JOURNAL: J. Lipid Res.

(D) VOLUME: 29

(E) ISSUE:

(F) PAGES: 1643 - 1649

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO
1488

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TGTCCCAAAG GCGGCTCCTA CGAGGCTGGC ATGGTGTGTC GCATCACCAG	50
GCCCCGCCCTC TTGGTGTGGA ACCAAGAGAC GSCCAAGGTG GTCCAGACGG	100
CCTTCAGCG CGCGGCTAT CCGGACGTCA GCGGAGAGAG GGCGGTGATG	150
CTCCTCGGCG GGGTCAAGTA CGGGCTGCAC AAGCTCCAGA TCAGCCACCT	200
GTGCATCGCC AGCAGCCAGG TGGAGCTGGT GGAGGCCAAG ACCATGAGG	250
TGGGCATCCA GAACGTGTCC GTGGTCTTCA AGGGGACCCCT GAACTACAGC	300
TACACGAGTG CCTGGGGGTT GGGCATCAAT CACTCTGTGG ACTTCGAGAT	350
CGACTCTGCC ATTSACCTCC AGATCAACAC ACAGGTGACC TGGGACGCTG	400
GCAGTGTGGG CACCAATGCC CCGGACTGCT AATGCGCTTT CCATAAGCTG	450
CTGCTGCACC TCCAGGGGGA GCGGAGCCG GGGTGGCTCA AGGAGCTCTT	500
CACAACTTC ATCTCTTCA CCGTGAAGCT GATTCTGAAG CGAGAGTTCT	550
GCAATGAGAT CAACACCATC TCCAACATCA TGGCTGACTT TGTCCAGAGG	600
AGGGCCGCCA GCATCCTCTC AGATGGAGAC ATGGGGGTGG ACATTCCCT	650
GAGGGGGGCC CCTGTCATCA CAGCCACCTA CTTGGAGTCC CATCACAAGG	700
GTCACTTCAC GCACAAGAAC GTCTCCGAGG CTTTCCCCCT CCGTGCCCTC	750
CCGCGCGGTC TTGTGGGGGA CTCCCGCATG CTCTACTTCT GGTTCCTCGA	800
TCAAGTGCTC AACTCCCTGG CCAGGGCCGC CTTCCAGGAG GSCGTGTGG	850
TGCTCAGCCT GACAGGGAT GAGTTCAAGA AASTCTTGA GAGGCAGGT	900
TTGACACCA ACCAGCAAT CTTCCAGGAG CTTTCCAGAG GGTTCACAC	950
CGGTCAGGCG CAGGTAGCG TCCACTGCCT TAAGGTGGCC AAGATCTCT	1000
GCCAGAACCG GGGTGTCTG GTGTCTTCTT CCGTCCCGCT GAGGTTCCT	1050
TTCCCCCGCC CAGATGGCG AGAAGCTGTG GCCTACAGGT TTCAGGAGGA	1100

TATCATCACC ACCGTCCAGG CCTCCTACTC GCAGAAAAAG CTCTTCCTAC 1190
 ACCTCTTGGA TTTCCASTGC GTGCGGGCCA GCGGAAB3GC AGGCAGGTCA 1200
 GCAAATCTCT CCGTGGGCGT CAGGACTGAG GCTAAGGCTG TTTCTAACCT 1210
 GACTGAGAGC CGCTCCGAGT CCCTGCAGAG CTCTCTCCGC TCCCTGATCG 1220
 CCACGJTGGG CATCCCGGAG GTCATGTCTC GGTTCGAGGT GGCSTTCACA 1230
 GGCCTCATGA ACAGCAAAGG CCGTGACCTC TTCGAAATCA TCAACCCCGA 1240
 GATTATCACT CTCGATGGCT GCGTGTCTGT GCAGATGGAG TTCGGTTTTC 1250
 CCAAGCACCT GCTGGTGGAT TTCCTGCAGA GCGTGAGC 1260

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 496 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(ix) FEATURE:

(A) NAME: Amino acid sequence for mature
rabbit CETP protein.

(B) LOCATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Nagashima, Mariko, et al

(B) TITLE: Cloning and mRNA tissue
distribution of rabbit
cholesteryl ester transfer
protein

(C) JOURNAL: J. Lipid Res.

(D) VOLUME: 29

(E) ISSUE:

(F) PAGES: 1643 - 1649

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:1 FROM 1 TO
496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Cys Pro Lys Gly Ala Ser Tyr Glu Ala Gly Ile Val Cys
 1 5 10

Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn Gln Glu
 15 20 25

Thr Ala Lys Val Val Gln Thr Ala Phe Gln Arg Ala Gly
 30 35

Tyr Pro Asp Val Ser Gly Glu Arg Ala Val Met Leu Leu

40

45

50

Gly Arg Val Lys Tyr Gly Leu His Asn Leu Gln Ile Ser
55 60 65

His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Asp
70 75

Ala Lys Thr Ile Asp Val Ala Ile Gln Asn Val Ser Val
80 85 90

Val Phe Lys Gly Thr Leu Asn Tyr Ser Tyr Thr Ser Ala
95 100

Trp Gly Leu Gly Ile Asn Gln Ser Val Asp Phe Glu Ile
105 110 115

Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Glu Leu Thr
120 125 130

Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys
135 140

Tyr Leu Ala Phe His Lys Leu Leu Leu His Leu Gln Gly
145 150 155

Glu Arg Glu Pro Gly Trp Leu Lys Gln Leu Phe Thr Asn
160 165

Phe Ile Ser Phe Thr Leu Lys Leu Ile Leu Lys Arg Gln
170 175 180

Val Cys Asn Glu Ile Asn Thr Ile Ser Asn Ile Met Ala
185 190 195

Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
200 205

Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro
210 215 220

Val Ile Thr Ala Thr Tyr Leu Glu Ser His His Lys Gly
225 230

His Phe Thr His Lys Asn Val Ser Glu Ala Phe Pro Leu
235 240 245

Arg Ala Phe Pro Pro Gly Leu Leu Gly Asp Ser Arg Met
250 255 260

Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn Ser Leu
265 270

Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser
275 280 285

Leu Thr Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln

290	295
Gly Phe Asp Thr Asn Gln Glu Ile Phe Gln Glu Leu Ser 300	305 310
Arg Gly Leu Pro Thr Gly Gln Ala Gln Val Ala Val His 315	320 325
Cys Leu Lys Val Pro Lys Ile Ser Cys Gln Asn Arg Gly 330	335
Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe 340	345 350
Pro Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe 355	360
Glu Glu Asp Ile Ile Thr Thr Val Gln Ala Ser Tyr Ser 365	370 375
Gln Lys Lys Leu Phe Leu His Leu Leu Asp Phe Gln Cys 380	385 390
Val Pro Ala Ser Gly Arg Ala Gly Ser Ser Ala Asn Leu 395	400
Ser Val Ala Leu Arg Thr Glu Ala Lys Ala Val Ser Asn 405	410 415
Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu 420	425
Arg Ser Leu Ile Ala Thr Val Gly Ile Pro Glu Val Met 430	435 440
Ser Arg Leu Glu Val Ala Phe Thr Ala Leu Met Asn Ser 445	450 455
Lys Gly Leu Asp Leu Phe Glu Ile Ile Asn Pro Glu Ile 460	465
Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met Asp Phe 470	475 480
Gly Phe Pro Lys His Leu Leu Val Asp Phe Leu Gln Ser 485	490
Leu Ser 495	

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:
      (A) NAME: Structural coding sequence for
              mature human CETP
      (B) LOCATION:
(x) PUBLICATION INFORMATION:
      (A) AUTHORS: Drayna, Dennis, et al.
      (B) TITLE: Cloning and sequencing of
                  human cholesteryl ester
                  transfer cDNA
      (C) JOURNAL: Nature
      (D) VOLUME: 327
      (E) ISSUE:
      (F) PAGES: 631 - 634
      (G) DATE: 18-JUN-1987
      (K) RELEVANT RESIDUES IN SEQ ID NO.3: FROM 1 TO
                                              1428

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGCTCCAAAG	GCACCTCGCA	CGAGGCAGGC	ATCGTGTCGC	GCATCAACAA	50
GGCTGCCCC	CTGGTGTTGA	ACCAAGAGAG	TGCACAGGTC	ATCCAGACCG	100
CGTTCCAGCG	AGCCAGCTAC	CCAGATATCA	CGCGGAGAG	GGCCATGATG	150
CTCCTTGCCC	AATCAAGTA	TGCTTTCCAG	AATATCCAGA	TCACCCACTT	200
GTTCATCGCC	AGCAGCCAGG	TGAGCTGGT	GGAGGCCAAG	TGCATTGATG	250
TTCGATTCA	GAACTGTGT	GTCTCTTCA	AGCGACCGT	GAAGTATGGC	300
TACACCATTC	CGTGGTGGT	GGTATTGAT	CATTCGATTG	ACTTCGAGAT	350
CGACTCTGCT	ATTGACCTCC	AGATCAACAC	ATAGCTCACC	TGTGACTCTC	400
GTAGAGTGCG	GACCGATGCC	CTGACTGCT	ACCTGTCTTT	CGATAAGCTT	450
CTCCTGCATC	TCCAAGGGGA	GCGAGAGGCT	GGGTGGATCA	AGCAGCTGTT	500
CACAAATTT	ATCTCCTTCA	CCCTCAAGCT	GGTCTGAAG	GGACAGATCT	550
GCAAGAGAT	CAAGCTCATC	TCTAACATCA	TGCTCCATT	TGTCCAGACA	600
AGGGCTGCCA	GCATCCTTT	AGATCCAGAG	ATTGCGCTCG	ACATTTCCCT	650
GACAGGTGAT	CCCGTCATCA	CAGCTCTCTA	CTTCGAGTCC	CATCAACAAG	700
GTCAATTCAT	CTACAAGAAT	GTCTCAGAGG	ACCTCCCTCT	CCGACCTTC	750
TGCGCCACAC	TGCTGGGGGA	CTCCCGCATG	CTGTACTTCT	GCTTCTCTGA	800
GCGAGTCTTC	CATCTGCTGG	CCAAGCTAGC	TTTCCAGSAT	GGTGGCTCA	850
TGCTCAGGCT	GATGGGAGAG	GAGTTCAAGG	CAGTCTCTGA	GAATTCAGGC	900

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TTCAACACCA ACCAGGAAAT CTTCGAAGAG GTTGTCGGCG GCTTCCCCAG      950
CCAGGCCCAA GTCAACGTCC ACTGCTCAA GATGCCCAAG ATCTCTGCCC      1000
AAAACAAGGG AGTCGTGGTC AATTCTTCAG TGATG3TGAA ATCTCTCTTT      1050
CCACGCCACAG ACCAGCAACA TTCTGTACCT TACACATTTG AAGAGGATAT      1100
CGTGACTACC GTTCAGGCTT CCTATTCTAA GAAAAAGCTC TTCTTAAGCC      1150
TCTTGGATTT CCAGATTACA CCAAAGACTG TTTCCAACTT GACTGAGAGC      1200
AGCTCCGAGT CCATCCAGAG CTTCCTGAG TCAATCATCA CGGCTGTGGG      1250
CATECCTGAG GTTATCTCTC GGCTCGAGGT AGTGTTTACA GGCCTCATGA      1300
ACAGCAAAGG CGTGAGCCTC TTCGACATCA TCAACCCCTGA GATTATCACT      1350
CGAGATGGCT TCCTGCTGCT GCAGATGGAC TTTGGCTTCC CTGAGCACCT      1400
GCTGCTGGAT TTCTTCAGA GCTTGAGC      1425

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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 476 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(ix) FEATURE:

(A) NAME: Amino acid sequence of mature human
 CETP

(E) LOCATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Drayna, Dennis, et al.
 (E) TITLE: Cloning and sequencing of human
 cholesteryl ester transfer cDNA
 (C) JOURNAL: Nature
 (D) VOLUME: 327
 (E) ISSUE:
 (F) PAGES: 632 - 634
 (G) DATE: 18-JUN-1987
 (K) RELEVANT RESIDUES IN SEQ ID NO:4: FROM 1 TO
 476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

Cys Ser Lys Gly Thr Ser His Glu Ala Gly Ile Val Cys
1           5           10

Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn His Gln
15           20           25

Thr Ala Lys Val Ile Gln Thr Ala Phe Gln Arg Ala Ser

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30

35

Tyr Pro Asp Ile Thr Gly Glu Lys Ala Met Met Leu Leu
40 45 50

Gly Gln Val Lys Tyr Gly Leu His Asn Ile Gln Ile Ser
55 60 65

His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Glu
70 75

Ala Lys Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val
80 85 90

Val Phe Lys Gly Thr Leu Lys Tyr Gly Tyr Thr Thr Ala
95 100

Trp Trp Leu Gly Ile Asp Gln Ser Ile Asp Phe Glu Ile
105 110 115

Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Gln Leu Thr
120 125 130

Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp Cys
135 140

Tyr Leu Ser Phe His Lys Leu Leu Leu His Leu Gln Gly
145 150 155

Glu Arg Glu Pro Gly Trp Ile Lys Gln Leu Phe Thr Asn
160 165

Phe Ile Ser Phe Thr Leu Lys Leu Val Leu Lys Gly Gln
170 175 180

Ile Cys Lys Glu Ile Asn Val Ile Ser Asn Ile Met Ala
185 190 195

Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
200 205

Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp Pro
210 215 220

Val Ile Thr Ala Ser Tyr Leu Glu Ser His His Lys Gly
225 230

His Phe Ile Tyr Lys Asn Val Ser Glu Asp Leu Pro Leu
235 240 245

Pro Thr Phe Ser Pro Thr Leu Leu Gly Asp Ser Arg Met
250 255 260

Leu Tyr Phe Trp Phe Ser Glu Arg Val Phe His Ser Leu
265 270

Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Met Leu Ser
275 280 285

Leu Met Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp
 290 295
 Gly Phe Asn Thr Asn Gln Glu Ile Phe Gln Glu Val Val
 300 305 310
 Gly Gly Phe Pro Ser Gln Ala Gln Val Thr Val His Cys
 315 320 325
 Leu Lys Met Pro Lys Ile Ser Cys Gln Asn Lys Gly Val
 330 335
 Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro
 340 345 350
 Arg Pro Asp Gln Gln His Ser Val Ala Tyr Thr Phe Glu
 355 360
 Glu Asp Ile Val Thr Thr Val Gln Ala Ser Tyr Ser Lys
 365 370 375
 Lys Lys Leu Phe Leu Ser Leu Leu Asp Phe Gln Ile Thr
 380 385 390
 Pro Lys Thr Val Ser Asn Leu Thr Glu Ser Ser Ser Glu
 395 400
 Ser Ile Gln Ser Phe Leu Gln Ser Met Ile Thr Ala Val
 405 410 415
 Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Val Phe
 420 425
 Thr Ala Leu Met Asn Ser Lys Gly Val Ser Leu Phe Asp
 430 435 440
 Ile Ile Asn Pro Glu Ile Ile Thr Arg Asp Gly Phe Leu
 445 450 455
 Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu
 460 465
 Val Asp Phe Leu Gln Ser Leu Ser
 470 475

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE:

- (A) NAME:
(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGGCGSCCA TGCAATACAT CAAGGCCAAT TCCAAGTTCA TGGGCATCAC 50
GGAGGCTTTC CCGCGCTCAG ATGGCGGAGA AGCTTGGCC TACAGCTTTC 100
AGGAGATAT CTTCGGTTTT CCGAAGCACG TGCTGGTGGA TTTCCTGCAG 150
AGCCTGAGCT AGCGGCCGC 169

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:
(A) NAME: Complementary strand to SEQ ID NO:5
(B) LOCATION: 1 to 169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCGGCGGCTA GCTCAGGCTC TGCAGGAAAT CCACCAGCAG GTGCTTGGGA 50
AAACCGAAGA TATCTCTCTC AAACCTGTAG GCCACAGCTT CTGGGCCATC 100
TGGGCGGGGG AAGCGCTCCG TGATGCCGAT GAACTTGGAG TTGGCCTTGA 150
TGTACTGCAT CCGCGGCCGC 169

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE: amino acid sequence of peptide encoded
by bases 10 to 159 of SEQ ID NO:5
(A) NAME:
(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile
1 5 10
Thr Glu Arg Phe Pro Arg Pro Asp Gly Arg Glu Ala Val
15 20 25

Ala Tyr Arg Phe Glu Glu Asp Ile Phe Gly Phe Pro Lys
30 35

His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
40 45 50

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(ix) FEATURE:

- (A) NAME: translational stop codon
- (B) LOCATION: 1606 - 1608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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GGCGCTGATG ATGTTGTTGA TTCTTCTAAA TCTTTTGTGA TGGAAAACTT      50
TTCTTGTGAC CACGGGACTA AACCTGGTTA TGTAGATTCG ATTCAAAAAG      100
GTATACAAAA GCCAAAATCT GGTACACAAG GAAATTATCA CGATGATTGG      150
AAAGGGTTTT ATAGTACCGA CAATAAATAC GACGCTGGGG GATACTCTGT      200
AGATAATGAA AACCGGCTCT CTGGAAAAGC TGGAGGCGTG GTCAAAGTGA      250
CGTATCCAGG ACTGACGAAG GTTCTCGCAC TAAAAGTGGG TAATGCCGAA      300
ACTATTAAGA AAGAGTTAGG TTTAAGTCTC ACTGAACCGT TGATGGAGCA      350
AGTCGGAAAG GAAGAGTTTA TCAAAAGGTT CGGTGATGGT GCTTCGGGTG      400
TAGTGCTCAG CCTTCCCTTC GCTGAGGGGA GTTCTAGGCT TGAATATATT      450
AATAACTGGG AACAGGCGAA AGCGTTAAGC GTAGAACTTG AGATTAATTT      500
TGAAACCGCT GGAAAACGTG GCCAAGATGC GATGTATGAG TATATGGCTC      550
AAGCCTGTGC AGGAAATCGT CTCAGGCGAT CAGTAGGTAG CTGATTGTCA      600

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TGCATAAATC TTGATTGGGA TGTCTAAAGG GATAAAACTA AGACAAAGAT 650
AGASTCTTTG AAAGAGCATG GGCCTATCAA AAATAAAATG AGCGAAAGTC 700
CCAATAAAAC AGTATCTGAG GAAAAAGCTA AACAATACCT AGAAGAATTT 750
CATCAAAACG CATTAGAGCA TCCTGAATTG TCAGAACTTA AAACCGTTAC 800
TGGGACCAAT CCTGTATTGG CTGGGGCTAA CTATGCGGGG TGGGCAGTAA 850
ACGTTGCGCA AGTTATCGAT AGCGAAACAG CTGATAATTT GGAAAAGACA 900
ACTGCTGCTC TTTCGATACT TCCTGSTATC GGTAGCGTAA TGGGCATTGC 950
AGACGGTGCC GTTCACCACA ATACAGAAGA GATAGTGGCA CAATCAATAG 1000
CTTATCGTC TTTAATGGTT GCTCAAGCTA TTCCATTGGT AAGAGAGCTA 1050
GTTGATATTG GTTTCGGTGC ATATAATTTT GTAGAGASTA TTATCAATTT 1100
ATTTCAAGTA GTTCATAATT CGTATAATCG TCCCCTGTAT TCTCCGGGCG 1150
ATAAAACGCA ACCATTTCTT CATGACGGGT ATGCTGTGAG TTGGAACACT 1200
GTTGAAGATT CGATAATCGG AACTGGTTTT CAAGGGGAGA GTGGGCACGA 1250
CATAAAAATT ACTGCTGAAA ATACCCCGGT TCCAATCGCG GGTGTCTTAC 1300
TACCGACTAT TCCTGGAAAG CTGGAAGTTA ATAAGTCCAA GACTCATATT 1350
TTCGTAAATG GTCCGAAAAT AAGGATGCGT TGCAGAGCTA TACAGGTTGA 1400
TGTAACTTTT TGTCGCCCTA AATCTCCTGT TTATGTTGGT AATGGTGTGC 1450
ATGCGAATCT TCACGTGGCA TTTCACAGAA GCAGCTCGGA GAAAATTCAT 1500
TCTAATGAAA TTTCGTGCGA TTCCATAGGC GTTCTTGGCT ACCAGAAAAC 1550

AGTAGATCAAC ACCAAGGTTA ATTCTAAGCT ATCGGTATTT TTTGAAATCA 1600

AAAGCTGA 1608

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 535 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE:
 - (A) NAME:
 - (B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly	Ala	Asp	Asp	Val	Val	Asp	Ser	Ser	Lys	Ser	Phe	Val	Met
1				5					10				
Glu	Asn	Phe	Ser	Ser	Tyr	His	Gly	Thr	Lys	Pro	Gly	Tyr	Val
15					20				25				
Asp	Ser	Ile	Gln	Lys	Gly	Ile	Gln	Lys	Pro	Lys	Ser	Gly	Thr
30					35				40				
Gln	Gly	Asn	Tyr	Asp	Asp	Asp	Trp	Lys	Gly	Phe	Tyr	Ser	Thr
45							50					55	
Asp	Asn	Lys	Tyr	Asp	Ala	Ala	Gly	Tyr	Ser	Val	Asp	Asn	Glu
60							65					70	
Asn	Pro	Leu	Ser	Gly	Lys	Ala	Gly	Gly	Val	Val	Lys	Val	Thr
75							80						
Tyr	Pro	Gly	Leu	Thr	Lys	Val	Leu	Ala	Leu	Lys	Val	Asp	Asn
85					90				95				
Ala	Glu	Thr	Ile	Lys	Lys	Glu	Leu	Gly	Leu	Ser	Leu	Thr	Glu
100						105					110		
Pro	Leu	Met	Glu	Gln	Val	Gly	Thr	Glu	Glu	Phe	Ile	Lys	Arg
115						120						125	
Phe	Gly	Asp	Gly	Ala	Ser	Arg	Val	Val	Leu	Ser	Leu	Pro	Phe
130							135					140	
Ala	Glu	Gly	Ser	Ser	Ser	Val	Gln	Tyr	Ile	Asn	Asn	Trp	Glu
145							150						
Gln	Ala	Lys	Ala	Leu	Ser	Val	Glu	Leu	Glu	Ile	Asn	Phe	Glu
155					160				165				
Thr	Arg	Gly	Lys	Arg	Gly	Gln	Asp	Ala	Met	Tyr	Gln	Tyr	Met

170	175	180
Ala Gln Ala Cys Ala Gly Asn Arg Val Arg Arg Ser Val Gly		
185	190	195
Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val Ile Arg		
200	205	210
Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly		
215	220	
Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val		
225	230	235
Ser Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln		
240	245	250
Thr Ala Leu Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val		
255	260	265
Thr Gly Thr Asn Pro Val Phe Ala Gly Ala Asn Tyr Ala Ala		
270	275	280
Trp Ala Val Asn Val Ala Gln Val Ile Asp Ser Glu Thr Ala		
285	290	
Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu Ser Ile Leu Pro		
295	300	305
Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala Val His		
310	315	320
His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser		
325	330	335
Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Gln Leu		
340	345	350
Val Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile		
355	360	
Ile Asn Leu Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro		
365	370	375
Ala Tyr Ser Pro Gly His Lys Thr Gln Pro Phe Leu His Asp		
380	385	390
Gly Tyr Ala Val Ser Trp Asn Thr Val Glu Asp Ser Ile Ile		
395	400	405
Arg Thr Gly Phe Gln Gly Glu Ser Gly His Asp Ile Lys Ile		
410	415	420
Thr Ala Glu Asn Thr Pro Leu Pro Ile Ala Gly Val Leu Leu		
425	430	
Pro Thr Ile Pro Gly Lys Leu Asp Val Asn Lys Ser Lys Thr		
435	440	445

His Ile Ser Val Asn Gly Arg Lys Ile Arg Met Arg Cys Arg
 450 455 460
 Ala Ile Asp Gly Asp Val Thr Phe Cys Arg Pro Lys Ser Pro
 465 470 475
 Val Tyr Val Gly Asn Gly Val His Ala Asn Leu His Val Ala
 480 485 490
 Phe His Arg Ser Ser Ser Glu Lys Ile His Ser Asn Glu Ile
 495 500
 Ser Ser Asp Ser Ile Gly Val Leu Gly Tyr Gln Lys Thr Val
 505 510 515
 Asp His Thr Lys Val Asn Ser Lys Leu Ser Leu Phe Phe Glu
 520 525 530
 Ile Lys Ser
 535

- (2) INFORMATION FOR SEQ ID NO:10
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL:
 - (iv) ANTI-SENSE:
 - (ix) FEATURE:
 - (A) NAME:
 - (B) LOCATION:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro
 1 5 10

Lys Val Ser Ala Ser His Leu Glu
 15 20